

**To:** Chiu, Weihsueh[WChiu@cvm.tamu.edu]  
**From:** Chiu, Weihsueh  
**Sent:** Mon 12/14/2015 4:22:07 PM  
**Subject:** My presentations from SRA  
Uncertainty and Variability - 21st Cent RA - WCHIU.PDF  
Dose Response integration and harmonization - V3 - WCHIU.PDF

Hello Colleagues,

Sorry about the mass e-mail. I have many cards/contacts from the meeting, and didn't remember who asked for which presentation. So I'm sending you all copies of both my Monday and my Wednesday presentation. Please don't hesitate to contact me with any questions or comments.

It was great to meet/see you all! Perhaps some of you I will see at SOT in March, where I'm scheduled to present at a CEC on population and genetic variability in risk assessment, as well as in a workshop session on probabilistic and Bayesian approaches to hazard characterization.

Finally, Greg Paoli and I are in the early stages of planning an SRA Workshop/Training on the WHO/IPCS probabilistic approach for next year's SRA that will include some hands-on exercises. Hope to see you there!

Regards,

Weihsueh

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**Sunday, March 13, 2016**

**PM10 CE Course: 1:15 PM–5:00 PM**

### **Genetics and Population Variability in Chemical Toxicity:**

#### **The What, the How, and So What?**

**ABSTRACT BODY:** The US EPA defines “variability” as “the range of toxic response or exposure - for example, the dose that might cause a toxic response can vary from one person to the next depending on factors such as genetic differences, preexisting medical conditions, etc.”

What are “genetic differences”? How do toxicologists and regulators estimate “population variability”? What new computational and experimental tools are available to substitute default “uncertainty factor” to account for variation in susceptibility among the members of the human population (i.e., inter-individual variability)? This continuing education course is designed to review basics of genetics and demonstrate how appreciation for the role of genetic variability and novel experimental and in silico models can become key elements in human health assessments of chemicals. By superimposing the opportunities that are now afforded by sequencing technologies and novel experimental models and data onto the risk assessment paradigm, this course will be informative to the risk assessment practitioners and the toxicology research community, and increase the scientific impact of the fundamental toxicology studies. In addition, this course is directly responsive to the new SOT Strategic Plan (2015-2018) and the Central Challenge of shaping the future of toxicology in a changing scientific landscape. By using case studies of how the scientific disciplines of genetics and toxicology intertwine, this course will strengthen the impact and relevance of toxicology.

Chair: Ivan Rusyn, Texas A&M University, College Station, TX

Co-Chair: Barbara Wetmore, The Hamner Institutes, Research Triangle Park, NC

## **SOT 2015**

### **Beyond Benchmark Dose: Advancing Probabilistic and Bayesian Approaches in Hazard Characterization**

Chairs: Nancy B Beck, American Chemistry Council (ACC) and Annie M. Jarabek, US EPA (EPA)

Workshop proposal

Potential Sponsors: RASS, RSESS

#### **Session Abstract:**

The National Academies (NRC), and other expert review bodies have frequently recommended that hazard assessments use Bayesian or probabilistic approaches in evaluating uncertainty and/or variability in hazard characterization. Most recently, in a 2014 review of EPA's Integrated Risk Information System (IRIS) program, the NRC reiterated their suggestion to use Bayesian analyses to inform quantitative judgments about hazard and dose-response. In this report, unlike other reports on the IRIS program, the NRC provided specific examples illustrating how such approaches could be incorporated. Similarly, the WHO/IPCS has also provided recent advice on using probabilistic approaches to characterize hazards in lieu of point estimates. In addition, computational approaches are progressing that provide for description of key events in a prognostic fashion that can facilitate the application of advances in systems biology as well as advancing meta-analysis and data integration. Such computational approaches offer the promise of network analyses and leveraging of new data streams in a read-across fashion. This workshop session will explore the recent recommendations provided by both NAS and WHO and will illustrate with case studies how these approaches as well as other probabilistic and Bayesian approaches can be implemented to inform hazard assessments.